



SEQUENCE LISTING

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<120> DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE
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<130> 19424PC

<140> 08/913,644

<141> 2001-09-17

<150> PCT/US96/03649

<151> 1996-03-18

<150> 08/408,669

<151> 1995-03-22

<150> 08/409,122

<151> 1995-03-22

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> HPV18 L1 Consensus Sequence

<400> 1

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agattattaa	ctgttggtaa	tccatatttt	agggttcctg	caggtggtgg	caataagcag	180
gatattccta	aggtttctgc	ataccaatat	agagtatttc	gggtgcagtt	acctgacca	240
aataaatttg	gtttacctga	taatagtatt	tataatcctg	aaacacaacg	tttagtgtgg	300
gcctgtgctg	gagtggaat	tggccgtggg	cagcctttag	gtgttggcct	tagtgggcat	360
ccattttata	ataaattaga	tgacactgaa	agttcccatg	ccgtacgtc	taatgtttct	420
gaggacgtta	gggacaatgt	gtctgtagat	tataagcaga	cacagttatg	tattttgggc	480
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tcacagggcg	attgcccccc	tttagaactt	aagaacacag	ttttggaaga	tggtgatatg	600
gtagatactg	gatatgggtg	catggacttt	agtacattgc	aagatactaa	atgtgaggta	660
ccattggata	tttgtcagtc	tattttgtaa	tatcctgatt	atttacaaat	gtctgcagat	720
ccttatgggg	attccatgtt	tttttgctta	cgacgtgagc	agctttttgc	taggcatttt	780
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aatttaacaa	tatgtgcttc	tacacagtct	cctgtacctg	ggcaatatga	tgctaccaa	1080
tttaagcagt	atagcagaca	tgttgaagaa	tatgatttgc	agtttatttt	tcagttatgt	1140
actattactt	taactgcaga	tgttatgtcc	tatattcata	gtatgaatag	cagtatttta	1200
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tttgataaat	ctgttgctat	tacctgtcaa	aaggatgctg	caccagctga	aaataaggat	1320
ccctatgata	agttaaagtt	ttggaatgtg	gatttaaagg	aaaagttttc	tttggactta	1380
gatcaatatc	cccttggaag	taaatttttg	gttcaggctg	gattgcgtcg	caagcccacc	1440
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1524

<210> 2

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<212> PRT

<213> Artificial Sequence

<220>

<223> HPV18 L1 Consensus Sequence

<400> 2

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Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
          35          40          45
Tyr Phe Arg Val Pro Ala Gly Gly Gly Asn Lys Gln Asp Ile Pro Lys
          50          55          60
Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro
65          70          75          80
Asn Lys Phe Gly Leu Pro Asp Asn Ser Ile Tyr Asn Pro Glu Thr Gln
          85          90          95
Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro
          100          105          110
Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp
          115          120          125
Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg
          130          135          140
Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly
145          150          155          160
Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys
          165          170          175
Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn
          180          185          190
Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met
          195          200          205
Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile
210          215          220          225
Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp
225          230          235          240
Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe
          245          250          255
Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro
          260          265          270
Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser
          275          280          285
Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser
290          295          300          305
Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn
305          310          315          320
Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr
          325          330          335
Thr Arg Ser Thr Asn Leu Thr Ile Cys Ala Ser Thr Gln Ser Pro Val
          340          345          350
Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val
          355          360          365
Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu
          370          375          380
Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu
385          390          395          400
Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Pro Thr Thr Ser Leu Val

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          405          410          415
Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp
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Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp
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Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro
          450          455          460
Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr
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<210> 3
 <211> 1389
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HPV18 L2 Consensus Sequence

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<400> 3
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gcagataaaa tattgcaatg gtcaagcctt ggtatatattt tgggtggact tggcataggt 180
actggaagtg gtacaggggg tcgtacaggg tacattccat tgggtgggcg ttccaataca 240
gttgtggatg tcggtcctac acgtcctcca gtggttattg aacctgtggg cccacagac 300
ccatctattg ttacattaat agaggactca agtgttgta catcagggtgc acctaggcct 360
acttttactg gcacgtctgg gtttgatata acatctgctg gtacaactac acctgcagtt 420
ttggatatca caccttcgtc tacctctgtt tctatttcca caaccaattt taccaatcct 480
gcattttctg atccgtccat tattgaagtt ccacaaactg gggagggtgc aggtaatgta 540
tttgttggtg cccctacatc tggaaacacat gggtatgaag aaataccttt acaaacattt 600
gcttcttctg gtacggggga ggaacccatt agtagtacc cttgcctac tgtgcggcgt 660
gtagcaggtc cccgccttta cagtagggcc taccaacaag tgtctgtggc taaccctgag 720
tttcttacac gtccatcctc ttttaattacc tatgacaacc cggcctttga gcctgtggac 780
actacattaa catttgagcc tcgtagtaat gttcctgatt cagattttat ggatattatc 840
cgtttacata ggctgcttt aacatccagg cgtggtactg tgcgctttag tagattaggt 900
caaagggcaa ctatgtttac ccgtagcggg acacaaatag gtgctagggt tcaactttat 960
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gcctcttcct atagtaatgt aacggtcctt ttaacctcct cttgggatgt gcctgtatac 1200
acgggtcctg atattacatt accacctact acctctgtat ggccattgt atcaccaca 1260
gccctgcct ctacacagta tattggtata catggtacac attattattt gtggccatta 1320
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<210> 4
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV18 L2 Consensus Sequence

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          20          25          30

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Ser	Leu	Gly	Ile	Phe	Leu	Gly	Gly	Leu	Gly	Ile	Gly	Thr	Gly	Ser	Gly
	50					55					60				
Thr	Gly	Gly	Arg	Thr	Gly	Tyr	Ile	Pro	Leu	Gly	Gly	Arg	Ser	Asn	Thr
65					70					75				80	
Val	Val	Asp	Val	Gly	Pro	Thr	Arg	Pro	Pro	Val	Val	Ile	Glu	Pro	Val
			85					90					95		
Gly	Pro	Thr	Asp	Pro	Ser	Ile	Val	Thr	Leu	Ile	Glu	Asp	Ser	Ser	Val
			100					105					110		
Val	Thr	Ser	Gly	Ala	Pro	Arg	Pro	Thr	Phe	Thr	Gly	Thr	Ser	Gly	Phe
	115						120					125			
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	210					215					220				
Arg	Leu	Tyr	Ser	Arg	Ala	Tyr	Gln	Gln	Val	Ser	Val	Ala	Asn	Pro	Glu
225					230					235					240
Phe	Leu	Thr	Arg	Pro	Ser	Ser	Leu	Ile	Thr	Tyr	Asp	Asn	Pro	Ala	Phe
			245						250					255	
Glu	Pro	Val	Asp	Thr	Thr	Leu	Thr	Phe	Glu	Pro	Arg	Ser	Asn	Val	Pro
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305					310					315					320
His	Asp	Ile	Ser	Pro	Ile	Ala	Pro	Ser	Pro	Glu	Tyr	Ile	Glu	Leu	Gln
			325						330					335	
Pro	Leu	Val	Ser	Ala	Thr	Glu	Asp	Asn	Gly	Leu	Phe	Asp	Ile	Tyr	Ala
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		355					360					365			
Ser	Ala	Val	Ser	Thr	Tyr	Ser	Pro	Thr	Ile	Ser	Ser	Ala	Ser	Ser	Tyr
	370					375					380				
Ser	Asn	Val	Thr	Val	Pro	Leu	Thr	Ser	Ser	Trp	Asp	Val	Pro	Val	Tyr
385					390					395					400
Thr	Gly	Pro	Asp	Ile	Thr	Leu	Pro	Pro	Thr	Ser	Val	Trp	Pro	Ile	Val
			405						410					415	
Ser	Pro	Thr	Ala	Pro	Ala	Ser	Thr	Gln	Tyr	Ile	Gly	Ile	His	Gly	Thr
			420					425					430		
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<223> oligonucleotide, antisense primer

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<223> oligonucleotide, antisense primer

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 <223> oligonucleotide, PCR primer

 <400> 15
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 <210> 16
 <211> 21
 <212> DNA
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 <220>
 <223> oligonucleotide, PCR primer

 <400> 16

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21